Ex 2 - Claudia and Maor

Q1

Imports

In [31]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import random
```

Let's create our data:

In [32]:
```
#Sample from normal distribution with 2 columns
def sample_normal(n, mu, sigma):
    return np.random.normal(mu, sigma, (n, 2))

data = pd.DataFrame(sample_normal(100, 5, 1), columns=['x', 'y'])
```

In [33]:
```
data
```

Out[33]:

	x	y
0	5.789838	4.328899
1	5.878885	4.105067
2	5.648813	3.602016
3	5.185626	4.980620
4	4.483713	6.503011
...	...	...
95	6.825994	3.960801
96	4.505771	4.791715
97	4.699218	4.002474
98	4.528350	3.249544
99	4.021845	2.504287

100 rows × 2 columns

First, let's form the sample covariance matrix:

In [34]:
```
def sample_covariance(data):
    #For each cell in data[0] and data[1], subtract the mean of the column:
    data_zero_mean = data.iloc[:,0] - data.iloc[:,0].mean()
    data_one_mean = data.iloc[:,1] - data.iloc[:,1].mean()
    X_tilde = np.array([data_zero_mean, data_one_mean])
    Sigma = np.dot(X_tilde, X_tilde.T) / len(data)
    return Sigma

def diagonalize(Sigma):
    eigvals, eigvecs = np.linalg.eig(Sigma)
    sorted_indices = np.argsort(eigvals)[::-1]
    sorted_eigvals = eigvals[sorted_indices]
    sorted_eigvecs = eigvecs[:, sorted_indices]
    D = np.diag(sorted_eigvals)
    return sorted_eigvecs, D
```

Let's diagonalze our sample_covariance with function and analytically

In [35]:
```
eigenvectors, D = diagonalize(sample_covariance(data))
```

In [36]:
```
eigenvectors
```

Out[36]:
```
array([[-0.39586454, -0.91830892],
       [-0.91830892,  0.39586454]])
```

In [37]:
```
D
```

Out[37]:
```
array([[1.25710438, 0.        ],
       [0.        , 0.7969257 ]])
```

Sanity check:

In [38]:
```
U = eigenvectors
Lambda = D
Sigma = U @ Lambda @ U.T
Sigma
```

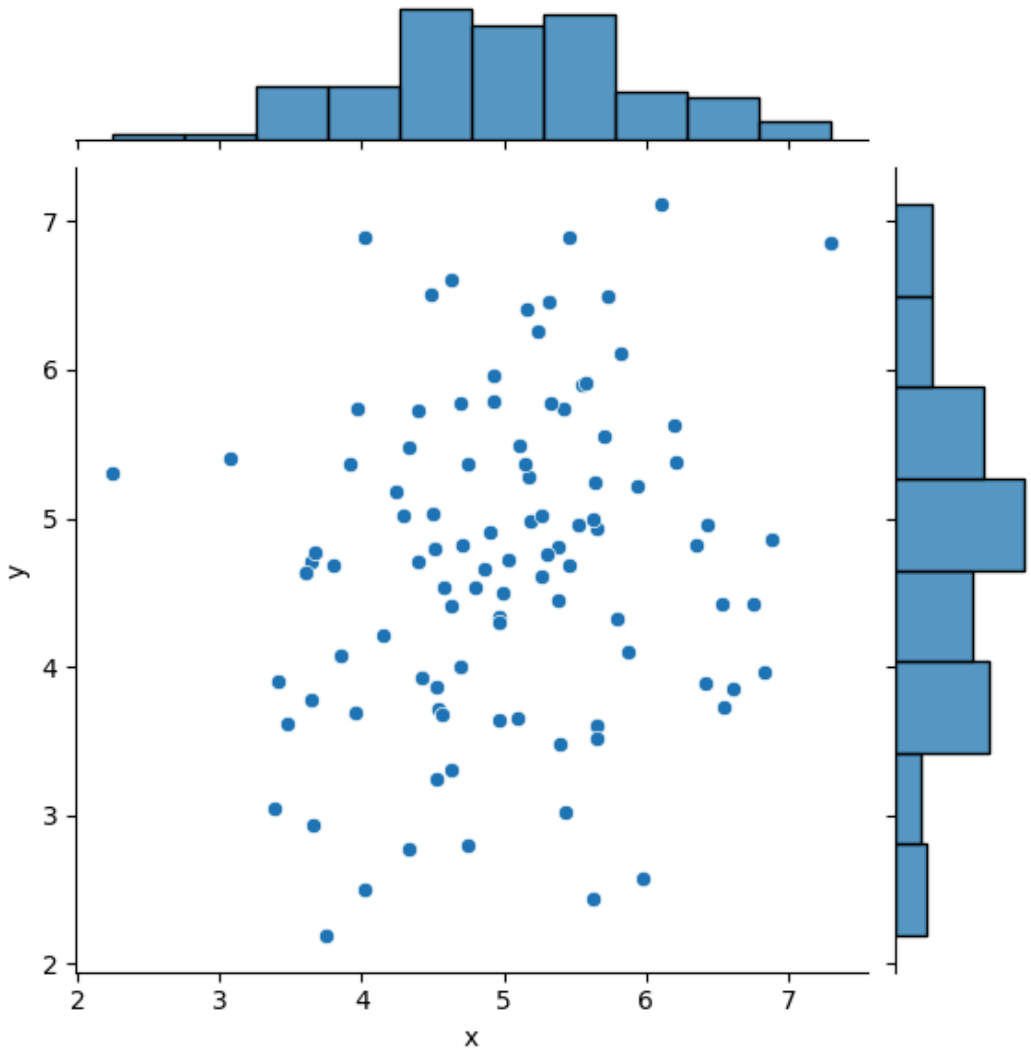
Out[38]:
```
array([[0.86903972, 0.16728688],
       [0.16728688, 1.18499036]])
```

In [39]:
```
sample_covariance(data)
```

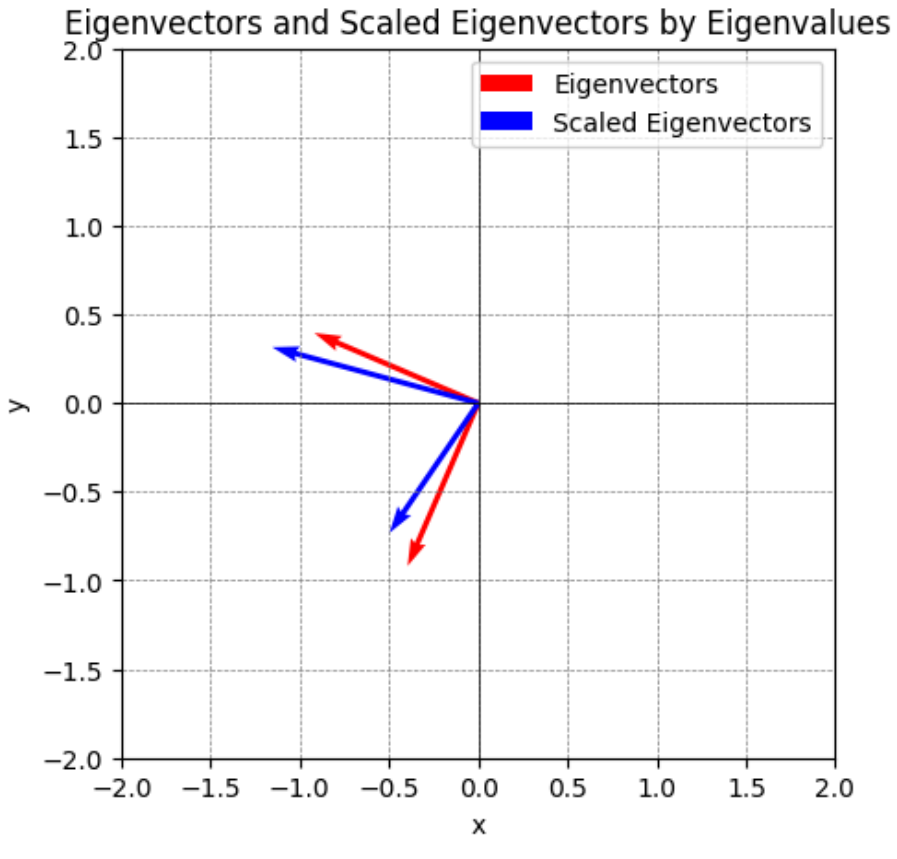
Out[39]:
```
array([[0.86903972, 0.16728688],
       [0.16728688, 1.18499036]])
```

They're equal!

In [40]:
```
import warnings
warnings.filterwarnings('ignore')
sns.set_style=('whitegrid')
plot = sns.jointplot(x=data['x'], y=data['y'], kind='scatter')
```



In [41]:
```
# Now draw the eigenvectors scaled by the eigenvalues using sns:

origin = np.array([[0, 0], [0, 0]])  # Origin point at (0,0)

# Plot
plt.figure(figsize=(5, 5))
plt.quiver(*origin, U[:, 0], U[:, 1], scale=1, color=['r', 'r'], angles='xy', scale_units='xy', label='Eigenvectors')

# Scale the eigenvectors by their eigenvalues
scaled_U = U * np.diag(D)

plt.quiver(*origin, scaled_U[:, 0], scaled_U[:, 1], scale=1, color=['b', 'b'], angles='xy', scale_units='xy', label='Scaled Eigenvectors')

# Plot settings
plt.xlim(-2, 2)
plt.ylim(-2, 2)
plt.axhline(0, color='black',linewidth=0.5)
plt.axvline(0, color='black',linewidth=0.5)
plt.grid(color = 'gray', linestyle = '--', linewidth = 0.5)
plt.xlabel('x')
plt.ylabel('y')
plt.title('Eigenvectors and Scaled Eigenvectors by Eigenvalues')
plt.legend()
plt.show()
```



Part 2

$$\tilde{X} := \tilde{X}_{i,j} = X_{i,j} - \frac{1}{n}\sum_{k=1}^{n} X_{k,j}$$

SVD decomposition of X tilde:

$$\tilde{X} = \tilde{U}\tilde{S}\tilde{V^T}$$

We got $\tilde{U}$ and $\tilde{V^T}$ **orthogonal**

Now we'll compute the **Sigma**:

$$\Sigma = \frac{1}{n}\tilde{X}^T\tilde{X} = \frac{1}{n}\tilde{V}\tilde{S}^T\tilde{U}^T\tilde{U}\tilde{S}\tilde{V^T} = \frac{1}{n}\tilde{V}\tilde{S}^2\tilde{V^T} = \tilde{V}(\frac{\tilde{S}^2}{n})\tilde{V^T}$$

Therefore, we got orthogonal $\tilde{V}$ multiplied by S^2 multiplied by $\tilde{V^T}$

Now, we chose $\tilde{V} = U$

From lecture 3 we know that S will have the square root of the $\tilde{X}^T\tilde{X}$ eigenvalues for cells $S_{i,i}$ for i = 1,2

We'll choose S^2/n as our diagonal matrix.

Lastly, we got the same composition as PCA immediately from SVD of $\tilde{X}$, where $S^2/n = \Lambda$

Part 3

We can see that for every matrix $\tilde{X}$ if we perform **PCA**, the PCA eigenvalues of $\tilde{X}$ will be equal to σ_i^2/n from the **SVD** of $\tilde{X}$.

Part 4

The relation is, as we've seen in part 2 that in the PCA decomposition the principle axes in U equal to $\tilde{V}$. We can understand that SVD and PCA are related and consequently, SVD is important

Part 5

In [42]:
```python
def Matrices(data):
    #For each cell in data[0] and data[1], subtract the mean of the column:
    data_zero_mean = data.iloc[:,0] - data.iloc[:,0].mean()
    data_one_mean = data.iloc[:,1] - data.iloc[:,1].mean()
    X_tilde = np.array([data_zero_mean, data_one_mean]).T
    Sigma = np.dot(X_tilde.T, X_tilde) / len(data)
    return Sigma, X_tilde,data_zero_mean

def diagonalize(Sigma):
    eigvals, eigvecs = np.linalg.eig(Sigma)
    sorted_indices = np.argsort(eigvals)[::-1]
    sorted_eigvals = eigvals[sorted_indices]
    sorted_eigvecs = eigvecs[:, sorted_indices]
    D = np.diag(sorted_eigvals)
    return sorted_eigvecs, D
```

In [43]:
```python
Sigma, X_tilde ,data_zero_mean = Matrices(data)
```

In [44]:
```python
U_tilde, sigma_tilde, V_t_tilde = np.linalg.svd(X_tilde)
```

In [45]:
```
V_t_tilde.T
```

Out[45]:
```
array([[ 0.39586454,  0.91830892],
       [ 0.91830892, -0.39586454]])
```

In [46]:
```
U, D = diagonalize(Sigma)
U
```

Out[46]:
```
array([[-0.39586454, -0.91830892],
       [-0.91830892,  0.39586454]])
```

We got that V = U up to numerical errors when searching for the right eigenvectors (the constant is different, in this case it's -1). The reason is that the computer searched for the right eigenvector using numerical method (For example, going through Gaussian distribution of potential eigenvectors) and every vector that multiplies the basis of the eigenspace by a constant can be an eigenvector.

In [47]:
```
D
```

Out[47]:
```
array([[1.25710438, 0.        ],
       [0.        , 0.7969257 ]])
```

In [48]:
```
np.sqrt(D*100)
```

Out[48]:
```
array([[11.21206662,  0.        ],
       [ 0.        ,  8.92706953]])
```

In [49]:
```
S = np.diag(sigma_tilde)
S
```

Out[49]:
```
array([[11.21206662,  0.        ],
       [ 0.        ,  8.92706953]])
```

Q2

Part 1

Let's look at the SVD Algorithm

In this algorithm we take matrix A and decompose it to 3 matrices: U,S,V*.

Therefore, In a backward - stable algorithm we would expect:

Let's assume

If we take $\tilde{A} = A + \Delta A$, such that $\Delta A \sim F(0, \sigma^2)$, For $\sigma^2 = \epsilon_{mach} \cdot ||A||$, Which satisfies:

For $SVD(\tilde{A}) = S\tilde{V}D(A), \quad ||\frac{\tilde{A}-A}{A}|| < O(\epsilon_{mach})$

Part 2

Let $A \in \mathbb{R}^{mxn}$

In the Full SVD if we take A, we get SVD(A) = USV*.

Now in this S we got from the algorithm, if $m \neq n$ we're going to get rows or columns of 0 values, depends on the shape of the original matrix (if m > n we get rows of 0 values in the last rows of S matrix, otherwise we get columns of 0 values in the last columns of S matrix).

We want to get:

$SVD(\tilde{A}) = \tilde{U}\tilde{S}\tilde{V}^* = S\tilde{V}D(A) = U \cdot (1+\delta_U)_{mxm} \cdot S \cdot (1+\delta_S)_{mxn} \cdot V^* \cdot (1+\delta_V)_{nxn}$, for $||\frac{\tilde{A}-A}{A}|| < O(\epsilon_{mach})$

We know that in the full SVD, we first take A*A, than diagonalize it and our V matrix is the diagonalizing matrix.

Then, in this decomposition we take the non negative eigenvalues and compute the square root of each one and these are our singular values.

If we insert to our SVD algorithm a matrix with pertubation, meaning $A + \Delta A$, it can affect drastically the matrices we're going to get.

Thus, we're comparing the accurate SVD on $\tilde{A}$ and the numerical SVD on A, which adds numerical error for each cell in the numerical U,S,V matrices.

We're not expecting the two terms to be equal and therefore the SVD is not backward stable.

Moreover,

Singular vectors (columns of U and V) can be highly sensitive to perturbations, especially when singular values are close to each other.

This sensitivity means that small changes in A can lead to large changes in $\tilde{U}$ and $\tilde{V}$. Thus, We'll expect to get: $SVD(\tilde{A}) \neq S\tilde{V}D(A)$

Part3

The advantages of the reduced form SVD and its potential backward stability are influenced by the rank r of the matrix:

Low Rank (r much smaller than min(m, n)): When the matrix A has a low rank, the reduced SVD captures the most important features of the matrix. The singular vectors and values retained in the reduced SVD are typically less sensitive to perturbations, leading to better backward stability.

high Rank (r close to min(m, n)): If the matrix has full rank, the reduced SVD is equivalent to the full SVD. In this case, the sensitivity issues and backward stability concerns of the full SVD apply. The advantage of the reduced form in terms of stability diminishes as r approaches the rank of the full matrix.

Furthermore, A matrix might be theoretically full rank, but if some singular values are very small, it behaves like a lower-rank matrix numerically. When computing the reduced SVD, the numerical rank (the number of nonzero singular values) determines the rank.

Still, the reduced SVD algorithm is still sensitive to small changes so we don't expect the accurate reduced SVD on A with added pertubation to be identical $U \cdot (1+\delta_U)_{mxm} \cdot S \cdot (1+\delta_S)_{mxm} \cdot V^* \cdot (1+\delta_V)_{mxm}$

Part 4

This means that there for every X theres $\tilde{X}$ which satisfies, for example for the full SVD:

$$\frac{||X-\tilde{X}||}{||X||} = O(\epsilon_{mach}) \quad \textbf{and} \quad \frac{||U \cdot (1+\delta_U)_{mxm} \cdot S \cdot (1+\delta_S)_{mxn} \cdot V^* \cdot (1+\delta_V)_{nxn} - \tilde{U}\tilde{S}\tilde{V}^*||}{||\tilde{U}\tilde{S}\tilde{V}^*||} = O(\epsilon_{mach})$$

This means the for every Matrix X we can find a matrix that is similar enough to it which suffices that the algorithm can yield accurate results numerically but we can have some errors up to epsilon machine, relative to the size of $\tilde{S}VD$

Q3

Part 1

In [50]:
```
import numpy as np

def lcg(m, a, c, n):
    s0_list = np.array([])
    s0 = random.randint(0, m)
    for i in range(n):
        s0 = (a * s0 + c) % m
        s0_list = np.append(s0_list, s0)
    return s0_list
```

In [51]:
```
A = [lcg(2**32, 22695477, 1, 10) for i in range(10)]
```

In [52]:
```
A = np.array(A)
A
```

Out[52]:
```
array([[3.26281218e+09, 1.35716539e+09, 3.37994081e+09, 3.08189133e+09,
        3.90908923e+09, 6.07548733e+08, 2.33942928e+09, 4.40194187e+08,
        9.93549000e+08, 5.47601257e+08],
       [2.67848488e+09, 2.41814002e+09, 2.41069010e+09, 2.92291537e+09,
        3.16430589e+09, 5.82495532e+08, 1.53280566e+09, 2.29081242e+09,
        3.20974705e+09, 1.92779524e+09],
       [2.53423765e+09, 4.19393502e+09, 5.97182570e+07, 1.56339594e+09,
        3.32110954e+09, 1.57714136e+09, 1.39382435e+09, 5.77905474e+08,
        2.40880248e+09, 4.45039976e+08],
       [3.60889153e+09, 3.13936727e+09, 1.88188988e+09, 9.50252901e+08,
        3.31633969e+09, 2.32034597e+09, 9.64384800e+07, 1.97071336e+09,
        2.16611239e+09, 2.34239994e+09],
       [3.54393366e+09, 8.41860758e+08, 3.16616322e+09, 2.71835804e+09,
        1.80720020e+09, 3.75245093e+09, 2.80357545e+09, 1.96457577e+09,
        9.44689401e+08, 4.78617998e+08],
       [2.59904128e+09, 2.02175252e+09, 3.34137964e+09, 3.15039197e+09,
        7.74713227e+08, 2.51167994e+09, 2.08025969e+09, 2.08987181e+09,
        3.69126818e+09, 2.69297152e+09],
       [3.15141761e+09, 3.64518458e+09, 2.18861595e+09, 3.87933785e+09,
        3.65402391e+09, 1.39459297e+09, 2.95863911e+09, 1.05360222e+09,
        2.09585920e+09, 1.93841602e+09],
       [3.95001945e+09, 3.13056934e+09, 1.58004092e+09, 9.15682542e+08,
        4.26950484e+09, 9.47502516e+08, 7.76543813e+08, 3.31548526e+09,
        2.35588335e+09, 3.06744018e+09],
       [1.30103291e+09, 1.69565089e+09, 2.92638067e+09, 4.73107020e+08,
        1.31571961e+09, 3.83076611e+09, 4.05979265e+09, 2.35679879e+09,
        4.76604393e+08, 5.73604158e+08],
       [3.87402976e+09, 3.44372310e+09, 1.07242164e+09, 4.69209045e+08,
        2.65012355e+09, 2.21031690e+09, 5.28902272e+08, 3.08141325e+09,
        2.78822572e+09, 1.54466398e+09]])
```

Part 2

In [53]:
```
def lcg_module4_reminder(m, n):
    a = random.randint(0, m)
    s0_list = np.array([a])
    s1_list = np.array([a])
    s0 = a
    s1 = a
    for i in range(n):
        s0 = s0 % 4
        s1 = np.floor(4 * s1 / m)
        s0_list = np.append(s0_list, s0)
        s1_list = np.append(s1_list, s1)
    return pd.DataFrame({'s0': s0_list,'s1':s1_list})
```

In [54]:
```
lcg_module4_reminder(100, 10)
```

Out[54]:

	s0	s1
0	68	68.0
1	0	2.0
2	0	0.0
3	0	0.0
4	0	0.0
5	0	0.0
6	0	0.0
7	0	0.0
8	0	0.0
9	0	0.0
10	0	0.0

We know that the second method is broken because of the following reasons:

First, let's look at $\lfloor 4s_n/m \rfloor$.

We want to get $\lfloor 4s_n/m \rfloor \leq 3 \Rightarrow 4s_n/m < 4$.

Therefore, we have to take $s_0 < m$ in order for the second method to work. But, in large number even this condition can fail.

THe reason is that floor function is not stable- it's highly sensitive to small change in decimal point.

M smaller than s_0:

In [55]:
```
def lcg_module4_reminder(m, n):
    a = 10
    s0_list = np.array([a])
    s1_list = np.array([a])
    s0 = a
    s1 = a
    for i in range(n):
        s0 = s0 % 4
        s1 = np.floor(4 * s1 / m)
        s0_list = np.append(s0_list, s0)
        s1_list = np.append(s1_list, s1)
    return pd.DataFrame({'s0': s0_list,'s1':s1_list})

lcg_module4_reminder(6, 10)
```

Out[55]:

	s0	s1
0	10	10.0
1	2	6.0
2	2	4.0
3	2	2.0
4	2	1.0
5	2	0.0
6	2	0.0
7	2	0.0
8	2	0.0
9	2	0.0
10	2	0.0

Numerically unstable:

In [56]:
```
def lcg_module4_reminder(m, n):
    a = 10**30
    s0_list = np.array([a])
    s1_list = np.array([a])
    s0 = a
    s1 = a
    for i in range(n):
        s0 = s0 % 4
        s1 = np.floor(4 * s1 / m)
        s0_list = np.append(s0_list, s0)
        s1_list = np.append(s1_list, s1)
    return pd.DataFrame({'s0': s0_list,'s1':s1_list})

lcg_module4_reminder(10**30  +5, 10)
```

Out[56]:

	s0	s1
0	10000000000000000000000000000000	10000000000000000000000000000000
1	0	4.0
2	0	0.0
3	0	0.0
4	0	0.0
5	0	0.0
6	0	0.0
7	0	0.0
8	0	0.0
9	0	0.0
10	0	0.0

Q4

Part 1

We'll draw 1000 sample of $(rcos\theta, rsin\theta)$,

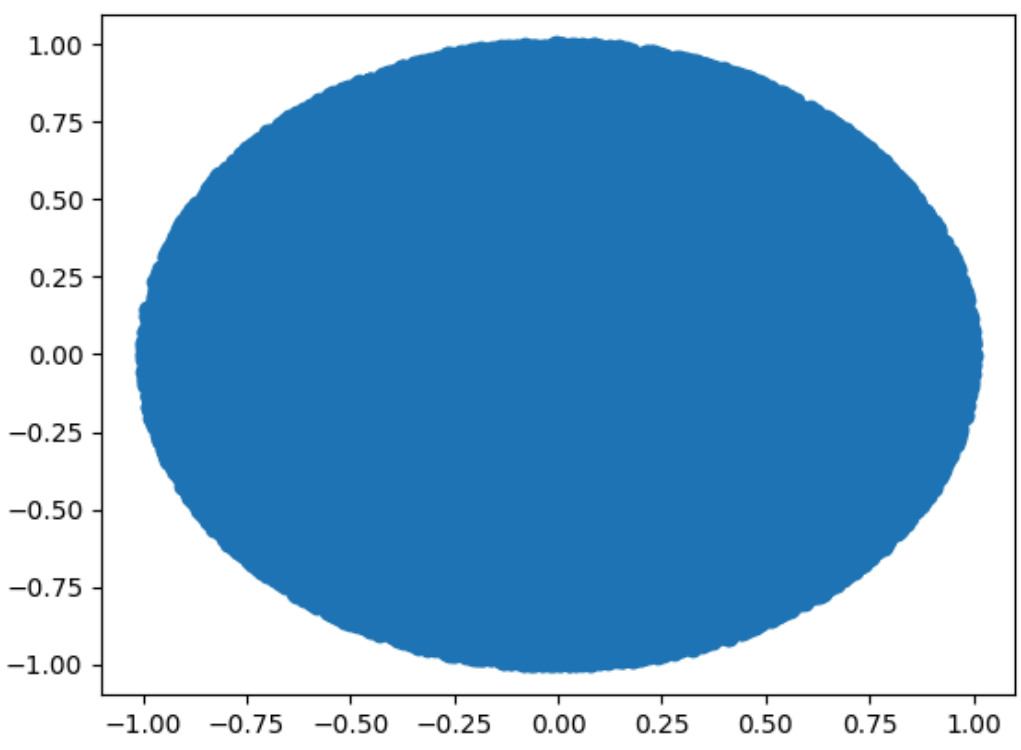
$r \sim U(0,1), \theta \sim U(0,2\pi)$

In [57]:
```
def Naive_sample_r_theta(n):
    r = np.random.uniform(0, 1, n)
    theta = np.random.uniform(0, 2*np.pi, n)
    x = r * np.cos(theta)
    y = r * np.sin(theta)
    print(sum(x**2 + y**2<=1))
    return plt.scatter(x, y)
    #return x, y

def PRNG_sample_r_theta(m,a,c,n):
    r = 0 + lcg(m, a, c, n)/m *1
    theta = 0 + lcg(m, a, c, n)/m * 2*np.pi
    x = r * np.cos(theta)
    y = r * np.sin(theta)
    return x,y
```

In [58]:
```
Naive_sample_r_theta(10**5)
```

```
100000
```

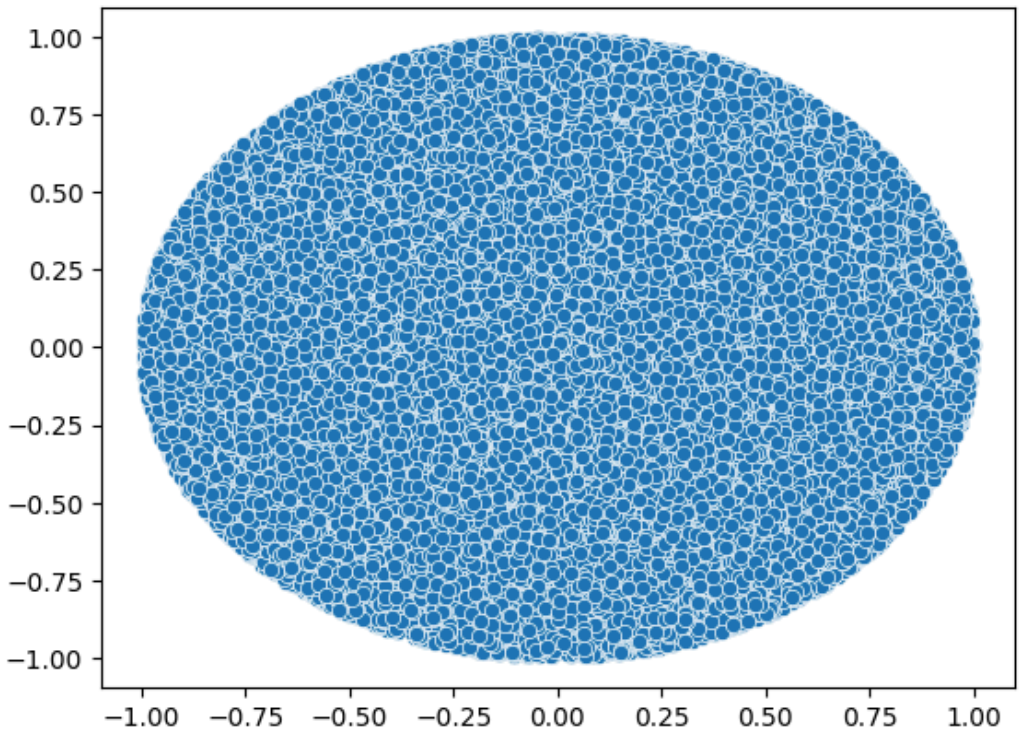
Out[58]: <matplotlib.collections.PathCollection at 0x1b9a1fda040>



In [59]:
```
x,y = PRNG_sample_r_theta(2**32, 22695477, 1, 10**5)
```

In [60]:
```
sns.scatterplot(x=x, y=y)
```

Out[60]: <AxesSubplot:>



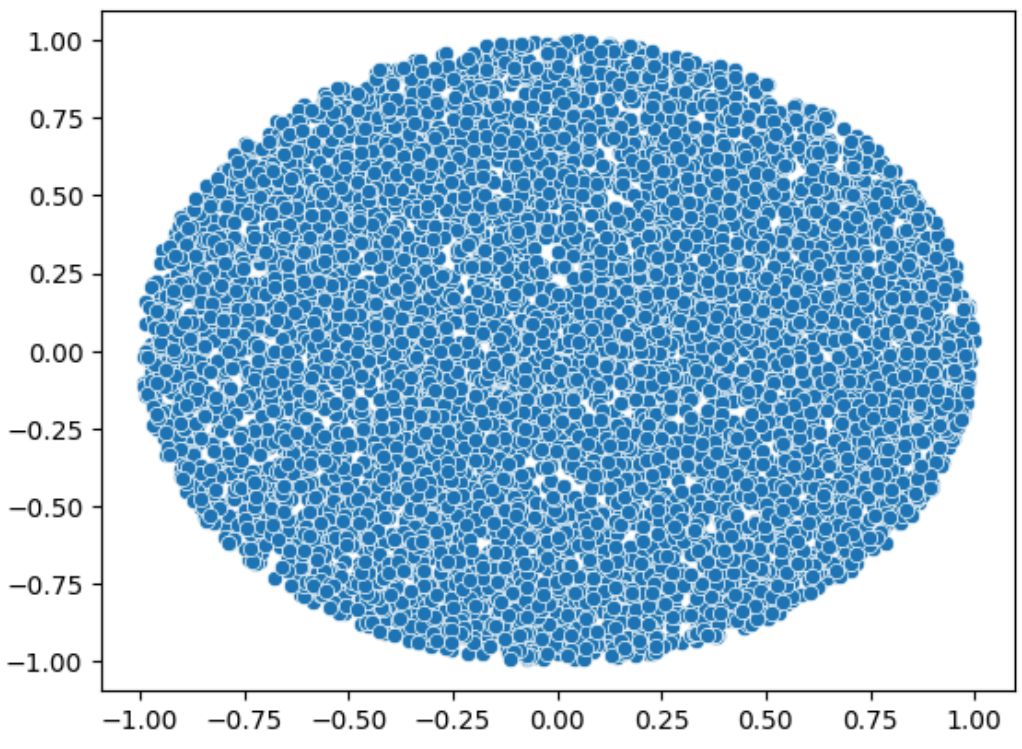
Part 2

In [61]:
```python
def unit_square_pick(m,a,c,n):
    x_list = np.array([])
    y_list = np.array([])
    for i in range(n):
        x =  -1 + lcg(m, a, c, 1)/m *2
        y = -1 + lcg(m, a, c, 1)/m *2
        # Make x,y 2d RV:
        xy = np.array([x, y])
        # Check if x,y is in the unit circle:
        if x**2 + y**2 <1:
            x_list = np.append(x_list, x)
            y_list = np.append(y_list, y)
    return x_list, y_list
```

In [62]:
```python
x_list, y_list = unit_square_pick(2**32, 22695477, 1, 10**4)
```

In [63]:
```python
sns.scatterplot(x=x_list, y=y_list)
```

Out[63]: <AxesSubplot:>



Part 3

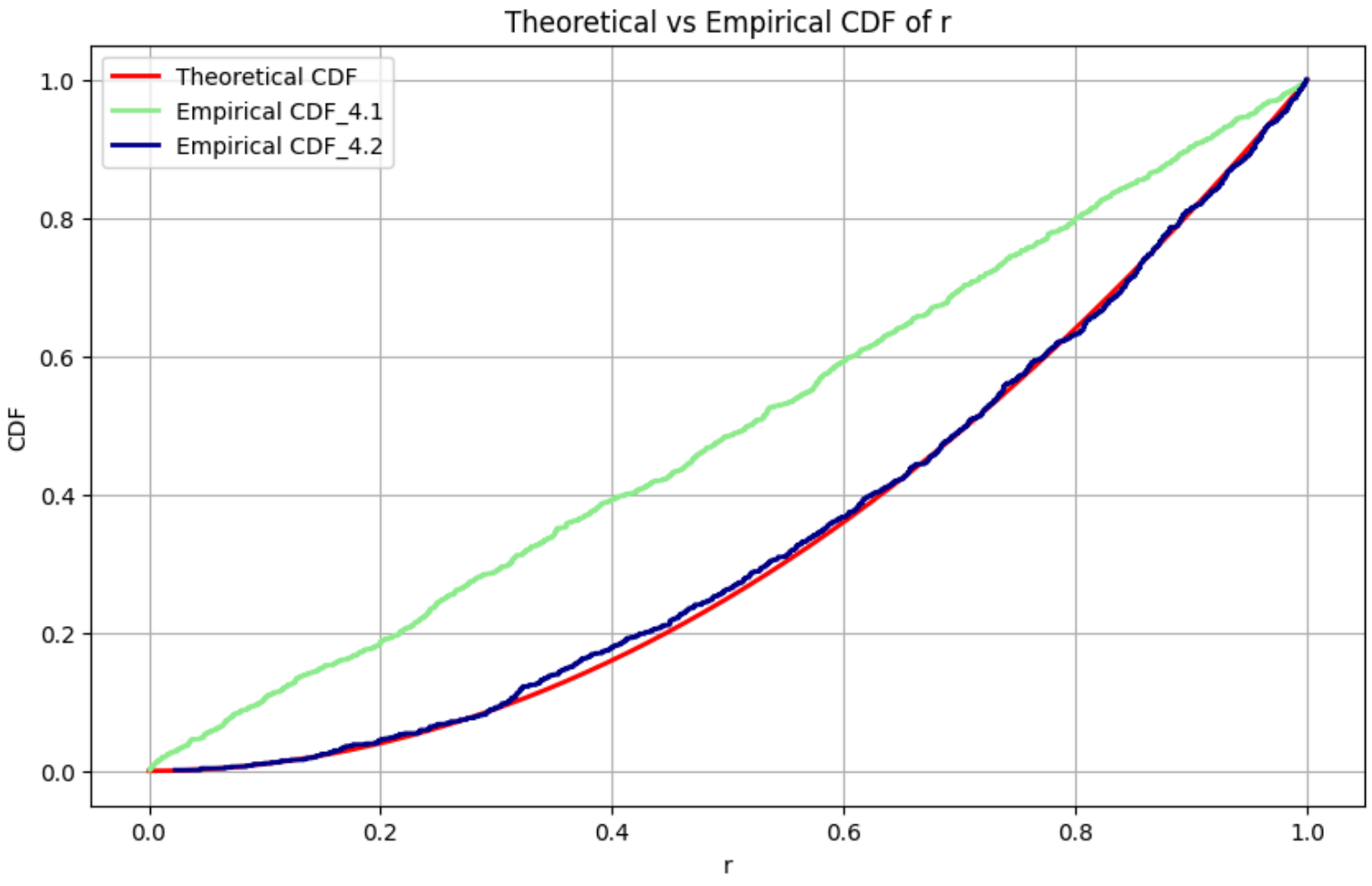
$$P(r \leq r_0) = \frac{\text{Area of smaller disk}}{\text{Area of unit disk}} = \frac{\pi r_0^2}{\pi \cdot 1^2} = r_0^2$$

We'll use both methods:

In [64]:
```python
def PRNG_sample_r_theta(m,a,c,n):
    r = 0 + lcg(m, a, c, n)/m *1
    theta = 0 + lcg(m, a, c, n)/m * 2*np.pi
    x = r * np.cos(theta)
    y = r * np.sin(theta)
    return x,y


def unit_circle(m,a,c,n):
    x_list = np.array([])
```

```
    y_list = np.array([])
    for i in range(n):
        x =  -1 + lcg(m, a, c, 1)/m *2
        y = -1 + lcg(m, a, c, 1)/m *2
        # Make x,y 2d RV:
        xy = np.array([x, y])
        # Check if x,y is in the unit circle:
        if x**2 + y**2 <= 1:
            x_list = np.append(x_list, x)
            y_list = np.append(y_list, y)
    return x_list, y_list
```

In [65]:
```
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import norm

# Set seed for reproducibility
np.random.seed(123)
n = 1000

x1,y1 = PRNG_sample_r_theta(2**32, 22695477, 1, n)
x2,y2 = unit_circle(2**32, 22695477, 1, n)
r1 = np.sqrt(x1**2 + y1**2)
r2 = np.sqrt(x2**2 + y2**2)

# Theoretical CDF function
def theoretical_cdf(r):
    return r**2

r1_sorted = np.sort(r1)
r2_sorted = np.sort(r2)

empirical_cdf1 = np.arange(1, len(r1_sorted) + 1) / len(r1_sorted)
empirical_cdf2 = np.arange(1, len(r2_sorted) + 1) / len(r2_sorted)


# Plotting
plt.figure(figsize=(10, 6))

# Plot theoretical CDF
r_vals = np.linspace(0, 1, 1000)
theoretical_vals = theoretical_cdf(r_vals)
plt.plot(r_vals, theoretical_vals, label='Theoretical CDF', color='red', linewidth=2)

plt.step(r1_sorted, empirical_cdf1, label='Empirical CDF_4.1', color='lightgreen', linewidth=2, where='post')
# Plot empirical CDF
plt.step(r2_sorted, empirical_cdf2, label='Empirical CDF_4.2', color='darkblue', linewidth=2, where='post')

# Add labels and title
plt.xlabel('r')
plt.ylabel('CDF')
plt.title('Theoretical vs Empirical CDF of r')
plt.legend()
plt.grid(True)

# Show plot
plt.show()
```



Part 4

Let X be a continuous real random variable with CDF F.

Let Y = F(X), we'll prove:

$Y \sim U(0,1)$

In other words, we'll show that P(Y<t) = t, for any $t \in [0,1]$

Let $t \in [0,1]$.

We know that for every CDF, F^{-1} is defined. So let's write the probability:

$$P(Y < t) = P(F(X) < t) = P(F^{-1}F(X) < F^{-1}(t)) = P(X < F^{-1}(t)) = F(F^{-1})(t) = t$$

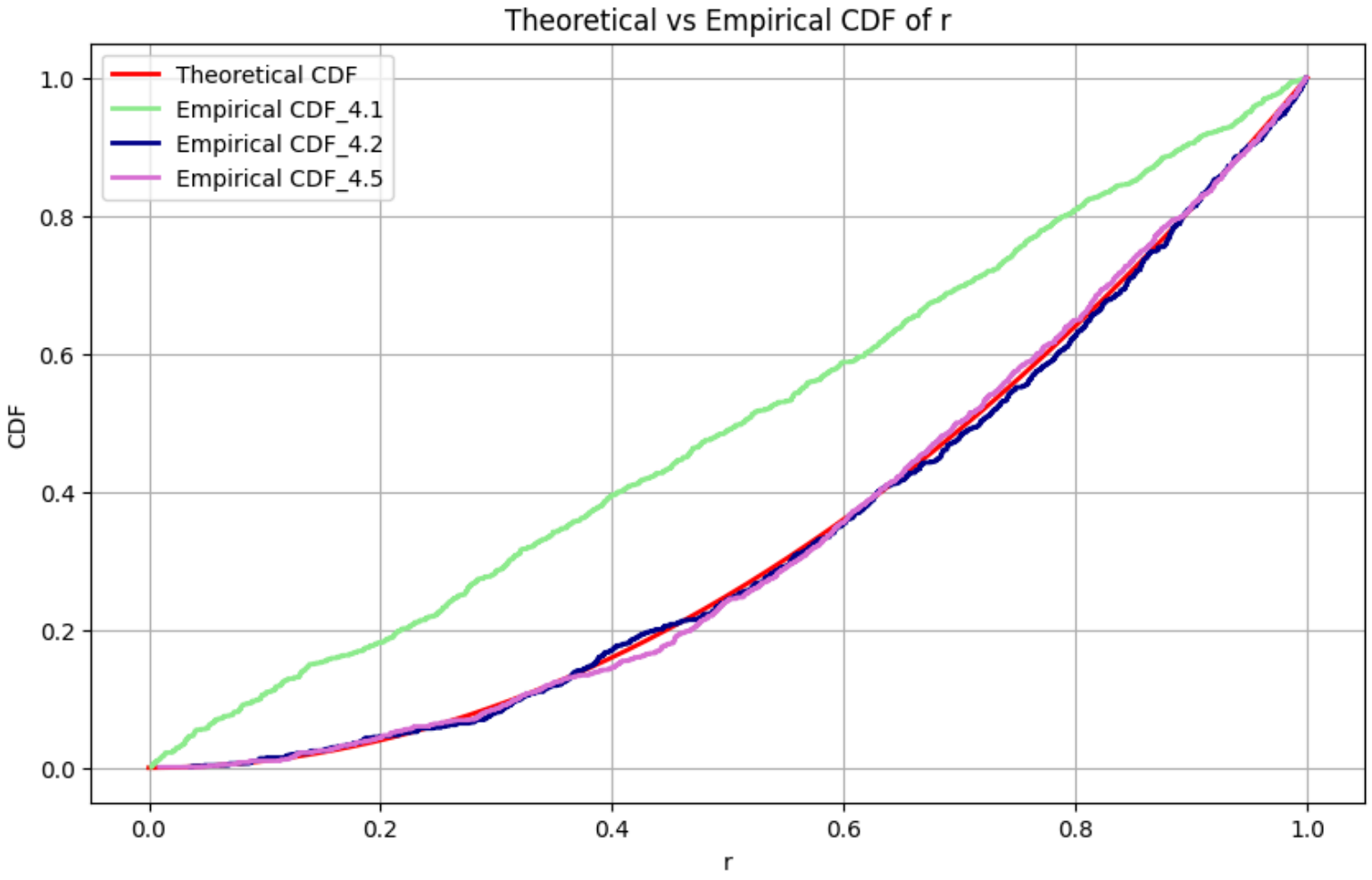
Therefore, Y distributes uniform with [0,1] because $t \in [0,1]$.

Part 5

We'll find function g such that r = g([U[0,1]]) and $\theta \sim U[0, 2\pi]$

So, from Part 4: we'll take $u \sim U[0,1]$ and we'll take $u = r^2 \Rightarrow u = \sqrt{r}$

In [70]:
```
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import norm

# Set seed for reproducibility
np.random.seed(123)
n = 1000

x1,y1 = PRNG_sample_r_theta(2**32, 22695477, 1, n)
x2,y2 = unit_circle(2**32, 22695477, 1, n)
u = np.random.uniform(0, 1, n)
r1 = np.sqrt(x1**2 + y1**2)
r2 = np.sqrt(x2**2 + y2**2)
r3 = np.sqrt(u)

# Theoretical CDF function
def theoretical_cdf(r):
    return r**2

r1_sorted = np.sort(r1)
r2_sorted = np.sort(r2)
r5_sorted = np.sort(r3)

empirical_cdf1 = np.arange(1, len(r1_sorted) + 1) / len(r1_sorted)
empirical_cdf2 = np.arange(1, len(r2_sorted) + 1) / len(r2_sorted)
empirical_cdf3 = np.arange(1, len(r5_sorted) + 1) / len(r5_sorted)

# Plotting
plt.figure(figsize=(10, 6))

# Plot theoretical CDF
r_vals = np.linspace(0, 1, 1000)
theoretical_vals = theoretical_cdf(r_vals)
plt.plot(r_vals, theoretical_vals, label='Theoretical CDF', color='red', linewidth=2)

plt.step(r1_sorted, empirical_cdf1, label='Empirical CDF_4.1', color='lightgreen', linewidth=2, where='post')
# Plot empirical CDF
plt.step(r2_sorted, empirical_cdf2, label='Empirical CDF_4.2', color='darkblue', linewidth=2, where='post')
plt.step(r3_sorted, empirical_cdf4, label='Empirical CDF_4.5', color='orchid', linewidth=2, where='post')

# Add labels and title
plt.xlabel('r')
plt.ylabel('CDF')
plt.title('Theoretical vs Empirical CDF of r')
plt.legend()
plt.grid(True)

# Show plot
plt.show()
```



It seems that with 2 methods we got decent results. The first method is less effective